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Result
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Maximum DB
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                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                 Score
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Gapop 10.0 ,
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3945
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Listing first 45 summaries
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ABP29047
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AAY00210
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1623.730 Million cell updates/sec
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                            Streptococcus poly
Streptococcus poly
Moraxella catarrha
Streptococcus equi
Moraxella catarrha
Enterococcus faeca
E faecalis EF104 a
                                                                                                                                                             Description
Enterococcus faeca
               faeca
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ABP29047
 Telford J,
Tettelin H;
                                                                                                                                                                                                             02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002 (first entry)
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taphylococcus	AAU37120	22	2344	3.7	144.5	Ů,
\circ	ABP56876	24	2283	3.7	144.5	
-	ABJ18914	24	2261	3.7	144.5	ω
Staphylococcus epi	AAW41602	19	1092	3.7	144.5	\sim
Listeria monocytog	ABB47334	23	940	3.7	144.5	_
-	AAY08603	20	11	3.7	145	٥
Collagen binding p	AAR22675	13	1185	3.7	146	w
Drosophila melanog	ABB58432	22	1563	3.7	147	ω
Staphylococcus aur	AAU37544	22	1349	3.7	147	7
Staphylococcus aur	AAU34402	22	1349	3.7	147	Οı
	ABU13740	24	2032		149	٠,
	ABU13738	24	2032		149	
us faec	ABU13736	24	2032		149	ω
	ABP43461	23	03	3.8	149	N
EF124	ABP43459	23	2032		149	_
77	ABP43457	23	2032		149	0
	AAY00242	20	2032		149	Ψ
	AAY00240	20	2032		149	w
Enterococcus faeca	AAY00238	20	2032		149	7
at	АВJ18969	24	1315		149	O١
S. aureus SdrD pro	AAY08642	20	1315		149	Oi
Streptococcal fibr	AAE22273	23	1161	3.8	150	
in-zein E	AAB72614	22	2537	3.9	152	w
dified Photor	AAB72611	22	2517		152	~
	ABG32651	23	2516		152	_
s tcdA	AAB72609	22	2516	3.9	152	0
Ð	AAW56572	19	2516		152	Ψ
rhabdus l	AAW17899	18	2516		152	w
Toxin TcdAil, enco	AAW56573	19	1849		152	7
	ABB47751	23	2013		152.5	٥١
7	AAW17900	18	1849		154	Ů,
	ABB47336	23	832		155	
	ABB47329	23	1530		156	ω
Listeria monocytog	ABB47333	23	1612		159	~
nterococcu	37	24	1448	4.1	161	
E faecalis EF104 p	ABP43429	23	1448	4.1	161	0

ALIGNMENTS

ABP29047 standard; Protein; 762

A

Streptococcus polypeptide SEQ ID NO 7270.

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.

Streptococcus pyogenes.

29-OCT-2001; 2001WO-GB04789

27-OCT-2000; 2000GB-0026333 24-NOV-2000; 2000GB-0028727 07-MAR-2001; 2001GB-0005640

(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.

Masignani V, Margarit Ros YI,

Grandi G,

Fraser C;

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CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus/GAS (Streptococcus/GAS), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.
CC willeic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to detect Streptococcus in a
CC biological sample. (I) is used to detect encoding (I), may be
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 3879; 4525pp; English.
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disease caused
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                  STLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMEDKKEVI
                                                                                                                            HIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHGFGDMND
                                                                                                                                                                                                                                  SQVYYCENADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDPDTFLK 480
                                                                                                                                                                                                                                                                                                                                                                                                               RVTQEAVWYYSDNAPISNPDESFKRESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSVKKWYKKHDGISTKFEDYAMSPRITGDELNQKLRAVMYNGHPQNANGIMEGLEPLNAI 180
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                                                                                                                                                                                                                                                                                                                                      TFKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGS
STLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMEDKKEVI
                                                                                                 HIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHGFGDMND
                                                                                                                                                                                                                                                                                                              TEKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVKKWYKKHDGISTKFEDYAMSPRITGDELNQKLRAVMYNGHPQNANGIMEGLEPLNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSD
                                                                                                                                                                                                       SQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDPDTFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVTQEAVWYYSDNAPISNPDESFKRESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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Pred. No. 2.4e-285;
; Mismatches 0;
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                                                       The invention relates to a protein (ABP25413-ABP30895) from group B CC streptcocccus/GBS (Streptcocccus agalactiae) or group A streptcocccus/GAS (Streptcocccus pyogenes), comprising one of 5483 sequences (S1), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptcocccus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptcocccus in a CC biological sample. (I) is used to determine whether a compound binds to CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be considered as a vaccine or diagnostic composition. The disease caused by Streptcocccus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity improved to the contract of the composition of the composition of the combinantly produce (I) and may be contracted to the composition of the combinantly produce (I) and may be contracted to the combinant of the contractors.
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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                        New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein - \,
                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes
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antiinflammatory; infection;
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                                                                                                                                                                                                                                                                                                                            Page 3880; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Η;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
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tococcus pyogenes; antibacterial;
vaccine; meningitis; gene therapy.
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284
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactoferrin receptor genes from Moraxella, especially M. catarrhalis - useful to diagnose Moraxella infection e.g. to detect otitis media due to M. catarrhalis infection and to immunise against such
                                                                                                                                                                                                                                                                                                               Sequence
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Misc-difference 296
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GDKYNKGYQNLLSGGL-----VPTKPPTPGDPPMPPNQPQTTSVLIRKYAIGDYSKL
                          YKHTPATYSVDFDQNTLKGKLSYYDNPNKQTADGRYIRSQFDTDKKVNEADVYEIDAKIN
                                                                                                                                         KNKKPGDDYQNIRFGYMELRELDLNKKGADTQSDKNRAIIFTTPTLFYHGENASTHLP--
                                                                                                                                                                    STK--FEDYA-----MSPRIT-----GDELNQKLRAVMYNG-----HPQNANGIMEGL
                                                                                                             EPLNAIRVTQEAVWYYSDNAPISNPDE-----SFKRESESNLVSTSQLSL----
                                                                                 ---KAGKFTDDKVGTYFNSTRKSNEGDKTDDKVGTYFNSTRKSNEGDLVSAAHIYLNSFK
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97US-0867941
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                                                                                                                                                                                                                                                                    4.6%; Score 181; DB 20; 20.7%; Pred. No. 0.00026;
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                                                     -MRQALKQLIDPNLATKMPKQVPDDF-----QLSIFESEDK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MS
                                                                                                                                                                                                                                                        Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                          Fibronectin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY90257;
                 N-PSDB;
                                                                                            (FRYK/)
                                                                                                                                         (GUSS/)
                                                                                                                                                                       22-DEC-1998;
                                                                                                                                                                                                    21-DEC-1999;
                                                                                                                                                                                                                                   29-JUN-2000
                                                                                                                                                                                                                                                                 WO200037496-A1
                                                                                                                                                                                                                                                                                              Streptococcus equi
                                                                                                                                                                                                                                                                                                                                                                      Streptococcus equi fibronectin binding protein, FNZ
                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY90257 standard; Protein;
                 2000-442641/38.
DB; AAA30874.
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                                                                                                                                         GUSS
                                                                                                                         LINDMARK H.
                                                                                           FRYKBERG L.
                                                                                                         JACOBSSON K
                                                            Lindmark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKIVLQQAKDKPYTAIHAKSYDHISFGEVLYNDNKGNPTRSYFVQGGQADVSTQLPSAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNRETGTAKSLIDDNTNTAPFVKELFSKKANDNNP--DPN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDSEGYKVKVNSQEVA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDIVFDI--KNGKIDGTGFTAKADVPNYREEVG----NNQGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDFHFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKVYHAGN----IRPEFENKYLPINEPTHEKTFALDGKNKAKFDVNFDTNSLTGKLNDER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEGATLQLTGDNVNSFQARVFSSNDI------GERIELSDGTYTLTELNSPAGYSIAEP
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                                                                                                                                                                                                                                                                                                                          respiratory
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                       98SE-0004491
                                                                                                                                                                                                      99WO-SE02448
                                                                                                                                                                                                                                                                                                                                          protein;
                                                              Jacobsson
                                                                                                                                                                                                                                                                                                                            ein; SFS; vaccine;
tract disease; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597
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                                                           Frykberg
                                                                                                                                                                                                                                                                                                                          equi
                                                                                                                                                                                                                                                                                                                                          horse;
                                                                                                                                                                                                                                                                                                                          e; strangles; t infection; FNZ
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                                                                                                                                                                                                                                                                                                                                      therapy;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                       468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                            NSQEVANATVSKTGITSDETLAFENNKEPVVPTGVDQK----INGYLALIVIAGISL
                                                                                                      KQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGL--PEGYSYLVKETDSEGYKVKV 690
                                                                                                                                                                      KYQSLIGTQWHPEDLVDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEIELKNN
                                                                                                                                                                                                                                                                                      DLFKYTVKPR-----DTDPDTFLKHIKKVIEKGYREKGQAIEYSGLTETQLRAATQ
                                                                                                                                                                                                                                                                                                                                                                                                                 GYSIAE----PIT-FKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTTON 407
                                                                                                                                                                                                   VMIGGQGQTIETTEDTQK---GMSGQSGGTIE----SEDTKKPEV-----
                                                                                                                                                                                                                              {\tt LAIYYFTDSAELDKDKLKDYHGFGDMNDSTLAVAKILVEYAQDSNPPQLTDLDFFIPNNN}
                                                                                                                                                                                                                                                               ESGETTPKPGQTGGQGPVIETTEDT------QKGMSGQSGGTIESENTKKPE
                                                                                                                                                                                                                                                                                                                                                      YAKFYYAKNKNGSSQVVYCFNADLKSPPDSEDGGKTMTPDFTTGEVKYTHIAG-----R 461
                                                                                                                                                                                                                                                                                                                                                                                      GLSGSEGKRDPLPGLKGEAGAPDT-----PQKPNDPL---QGLEGGN-----SPIVEQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLIRKYAIGDYSKLLEGATLQLTGDNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSKL-KSEQSNYSLDIYVYQSGGHDHMKDYQNLLGSTLIPKEPLKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLNNDSSRKVTQLAIWYFSD----SLTKEYLKDTGGYNL----NDMEKKALDFLISKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEYRWYGYESYVR-GHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSDSSVKKW
                                                                                                                                         ---MIGGQ
                                                                                                                                                                                                                                                                                                                         YGS---TEGYHGQSGILE--ETEDTNPPGIILGGSGNVE--THEDTRNPHLMGIGGGLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATKMPKQVPDDFQLSIFESEDKGDKYNKGYQNLLSGGLVPTKPPTPGDPPMPPNQPQTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LEPLNAIRVTQEAVWYYSDNAPISNPDESFKRESESNLVSTSQLSLMRQALKQLIDPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDIRSPYNDLPVYEKKLGYDGIFKQYAPDYKKDISDIASALVAVLSNGYPTNKSQLSTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEQLYYGWNDGTRQSSPYF--LYVSPKNAPKRELKDEYVVYCFNKKLYWPDQWESIYSNF
                                                                           KSEII---IGGQGQIIDFSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -YKKHDGISTKFEDYAMSPRITGDELNQKLRAVMYNGHPQNANGIMEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GHNGNGLSGLEGGSSGSQETNE--DGKKGL--IGFHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
               DE----KPNKGTHLPQTSDMKQLTLSIIGAMSMLLVLCLSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 180; DB 21;
Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                       GQIIDESEN -- TQSGMSGQSGDTT ----
                                                                           TQPGMSGQSGGTTIVEDTKKPTPKPKP
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572

429

467

383

330

284

292

149 173 89

245

Length 597, Indels

Gaps

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RESULT 5
AAW89413
ID AAW89413
AC AAW89413
AC AAW89413
AC AAW89413
AC AAW89413
AC AAW89413
AC AAW8941
DT 21-J
DE MOTA
XXX Lact
KW Lbact
KW Pneu
KW Vacc
OSS MOTA
XXX VACC
PT ALSC
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Best Local :
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                                                                                                                                                                                                                                                                                           This protein comprises lactoferrin binding protein 2 (Lbp2) of of Moraxella catarrhalis (Branhamella catarrhalis) 4223. It is encoded by the lbpB gene of the lactoferrin receptor (1fr) locus (see AAV72019) identified in the M. catarrhalis 423 genome. Immunogenic compositions, including vaccines, based upon expressed recombinant Lbpl and/or Lbp2 and/or ORF3 proteins (see AAW89413-21), portions of these, or their analogues, can be prepared for prevention of diseases caused by Moraxella. M. catarrhalis is a causative agent of otitis media and has been associated with sinusitis, conjunctivitis and inflammatory diseases of the lower respiratory tract, such as pneumonia, chronic bronchitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 2; 202pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactoferrin receptor genes from Moraxella, especially M. catarrhalis - useful to diagnose Moraxella infection e.g. to detect otitis media due to M. catarrhalis infection and to immunise against such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1998;
03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactoferrin receptor; lactoferrin binding protein; Lbp2; lbpB gene; infection; otitis media; sinusitis; conjunctivitis; pneumonia; bronchitis; tracheitis; emphysema; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis lactoferrin binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW89413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW89413 standard; Protein;
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                                                                                                                                                                               Similarity
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                                                                                                                  TRFPNKLNTLNTQRVLSKNSKRFTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTPNAIN
PDYSNDLVQQWQGKLYVGIDAHRPDGIGTGKNLRQPITANDIKPLYFNKFPALSDLHLDS
                                        PDSSSE--YRWYG--YESYVRGHP-----
                                                                               TTDPNGDNNQLTQ-----AQKTAAAAGFFVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catarrhalis
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97US-0867941
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/note= "c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note "encoded by AAR"
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                                                                                                                                                           Score 178; DB 20;
Pred. No. 0.00043;
8; Mismatches 305
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                                                                                                                                                                                                                                        standard;
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                    faecalis
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Enterococcus faecalis; 1 detection; attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTVXTDXTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDSEGYKVKVNSQEVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDMNDSTLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMED
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                                                                                                                                                                                                                                                                                                                                               QLQYDKGDGINDTAEKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         GFTAKADVPNYREEVG----NNQGG-----
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                                                                           faecalis antigenic polypeptide fragment EF104
                                                                                                                          (first entry)
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                           infection;
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                           vaccine;
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                           immune response; diagnosis;
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Enterococcus faecalis polynucleotides - usproducts for the detection of Enterococcus and for use for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN
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                                                                                               TVTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV
                                                                                                                                                                                            LTG-----DNVNSFQARVESSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAG
                                                                                                                                                                                                                                YWDRGQYFDKPMTPNSPGYPTITFDENTNSYTFDFGKTNKRYII-EYKNANGWIDVPTLY
                                                                                                                                                                                                                                                                                                                              RESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQVPDDFQLSIFESEDKGDKYNKGYQN
                                                                                                                                                                                                                                                                                                                                                                VIKETTPITNEIQIPIGFNYVPDSLPKDKSIPVDTIPITMSAEGLTPVDTTVTT---NSK
                                                                                                                                                                                                                                                                                                                                                                                              ELNQKLRAVMYNGHPQNANGIMEGLE-----PLNAIRVTQEAVWYYSDNAPISNPDESFK
                                                                                                                                                                                                                                                                                                                                                                                                                                TTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYYK----LGT---DYTVTPTSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VNLEGSRSYQYYCFNLKKAFP----LGSDSSYKKWYKKHDGISTKFEDYAMSPRITGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ-----NGAYSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALVTSMVGAKTVFGLVES---STPNAINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLR
                                                              YCFNADLKSPPDSEDGGKTMTPDFTTGE---VKYTHIAGRDLFKYTVKPRDTDPDTFLKH
                                                                                                                               KVYT-IIDGK--QIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVV 424
                                                                                                                                                                                                                                                             LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI----RKYAIGDYSKL---LEGATLQ
                                                                                                                                                                                                                                                                                             RGSERTLQSSKNQFLVNARNDSFDSLSVRTKIPAGA--DVLFDIYDVSN--DQVDSIYPQ
                                                                                                                                                               ITGTAKEPQSNNNEGSASVSVQN---EALDILSAT-----QAANPTLKNVTKT
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97US-0044031.
97US-0046655.
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                                -SLEKTTNGAKVIFKDYTLTENITIEYNTVSANAGQIYTETTIDSETLNQMSA
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21.18;
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EKGYREKGQAIEYSGLTETQLRAATQLAIYYFTD--
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                       Query Match
Best Local S
Matches 159
                                                                                                                                                                                                               vaccines
a member
faecalis
                                                                                               The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faccalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a protein of the invention.
                                                                         Sequence
                                                                                                                                                                                      Claim 9; Page 185;
                                                                                                                                                                                                                         New genes and polypeptides from Enterococcus faecalis, useful vaccines for preventing, treating or attenuating an infection a member of the Enterococcus genus in an animal, particularly
                                                                                                                                                                                                                                                                                                                                                                04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 faecalis
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                                                                         AA;
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                                                                                                                                                                                      255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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                       Score 161; DB
Pred. No. 0.01
04; Mismatches
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SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ-----

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  06-MAY-1997;
16-MAY-1997;
14-NOV-1997;
14-NOV-1997;
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                                                                                                                                      04-MAY-1998
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97US-046655P.
97US-066009P.
97US-066099P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotide fragments of a gene from Enterococcus faecalis, EF040, and the polypeptides encoded by them. The polypeptides are useful in detecting E. faecalis, as epitope tags, as molecular weight markers on SDS-PAGE gels or for molecular sieve gel filtration columns, in generating antibodies that specifically bind to the E. faecalis polypeptides, in generating an immune response against E. faecalis and other Enterococcus species and as vaccines against other bacterial genera. The polynucleotides are useful as probes for gene mapping and for identifying E. faecalis in biological samples. Sequences ABU13508-ABU3755 represent EF040 polypeptides of the invention. Note: The sequence data for this patent can also be obtained from USPTO at sequence approved approximate the sequence of the sequence contains a sequence of the seque
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DB; ABX61756.
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59; Conservative 104;
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                                                                         DKDKLKDYHGFGDM-NDSTLAVAKILVEYAQDSNPPQLT-----DLDFFIP----
                                                                                                                                 SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF
                                                                                                                                                                                                                                         Y-----SLEKTTNGAKVIFKDYTLTENITIEYNTVSANAGQIYTETTIDSETLNQMSA
                                                                                                                                                                                                                                                                                              YCFNADLKSPPDSEDGGKTMTPDFTTGE----VKYTHIAGRDLFKYTVKPRDTDPDTFLKH
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Pred. No. 0.017;
)4; Mismatches 326;
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Matches 159
                                                                                                                                                                 The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins can and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                          New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis; 1
detection; attenuation;
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                         SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ-----NGAYSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PITYSDEGKETAYUTVKPDQSKLEVKD--TTTYV--GDSWK----PE--DNFVSATDK 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALVTSMVGAKTVFGLVES----STPNAINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLR
--VNLEGSRSYQVYCFNLKKAFP----LGSDSSVKKWYKKHDGISTKFEDYAMSPRITGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHSRLQVKDSTIYVGDSWKPEE--NFVSATDKTGQDVPFE----KITVSGQVDNXKAGV
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                                                                                                                               1448
                                                                                                                                                                                                                                                                                                                                                                                                                     Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                faecalis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   faecalis
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Hromockyj A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigenic
                                                                            104;
                                                                           Score 161; DB 20;
Pred. No. 0.017;
04; Mismatches 326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune
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                                                                                                    Length 1448
                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                          vaccines
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RESULT 10
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Choi GH,
                                                                                                                                                                                                                      E faecalis EF104 protein.
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                                                       04-MAY-1998;
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                                                                                                           18-APR-2002
                                                                                                                                     US2002045737-A1
                                                                                                                                                                Enterococcus
                                                                                                                                                                                            Enterococcus;
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                          (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI-----RKYAIGDYSKL---LEGATLQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYYK----LGT---DYTVTPTSDGS 611
                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                YPIIYSDEGKEETAYVTVKPDQSKLEVKD--TTIYV--GDSWK----PE--DNFVSATDK 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVYT-IIDGK--QIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIKETTPITNEIQIPIGENYVPDSLPKDKSIPVDTIPITMSAEGLTPVDTTVTT----NSK
                                                                                                                                                                                                                                                                                                                                                                                                  EGYKV---KVNSQEVANATVSKTGITSDETLAFEN 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHSRLQVKDSTIYVGDSWKPEE---NFVSATDKTGQDVPFE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNNKYQ-----SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLRKTVTGLAGDRTKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE--YLTGKAIKLVKGDNQLKIPLTKTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGSERTLQSSKNQFLVNARNDSFDSLSVRTKIPAGA--DVLFDIYDVSN--DQVDSIYPQ
 Bailey C,
                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                 faecalis
                                                                                                                                                                                           vaccine;
                                                       98US-0071035
                                                                                98US-0071035
                                                                                                                                                                                                                                                                                                        Protein;
Hromockyj A,
                            SCI INC
                                                                                                                                                                                            gastrointestinal
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 Kunsch
                                                                                                                                                                                            disease;
 CA;
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Best Local S
Matches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of polypeptides from Entercoccus faecalis. The proteins can be used as vaccines for preventing or an an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 182-183;
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DB; ABN98185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the Enterococcus genus in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s and polypeptides from Enterococcus faecalis, useful for preventing, treating or attenuating an infection of the Enterococcus genus in an animal, particularly
                                                                                                                                                                                                                                                                                                                                              KVYT-IIDGK--QIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYYK----LGT---DYTVTPTSDGS
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                                                        HFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDS
                                                                                                                  NNNKYQ-----SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLRKTVTGLAGDRTKDF
                                                                                                                                              TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE - - YLTGKAIKLVKGDNQLKIPLTKTI
                                                                                                                                                                           DKDKLKDYHGFGDM-NDSTLAVAKILVEYAQDSNPPQLT-----
                                                                                                                                                                                                         SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF
                                                                                                                                                                                                                                   IKKVI-----EKGYREKGQAIEYSGLTETQLRAATQLAIYYFTD----SAEL
                                                                                                                                                                                                                                                                Y-----SLEKTTNGAKVIFKDYTLTENITIEYNTVSANAGQIYTETTIDSETLNQMSA
                                                                                                                                                                                                                                                                                             YCFNADLKSPPDSEDGGKTMTPDFTTGE----VKYTHIAGRDLFKYTVKPRDTDPDTFLKH
                                                                                                                                                                                                                                                                                                                         TVTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV------KGVPEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI----RKYAIGDYSKL---LEGATLQ
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 EGYKV --- KVNSQEVANATVSKTGITSDETLAFEN
                             YPIIYSDEGKEETAYVTVKPDQSKLEVKD--TTIYV--GDSWK---
                                                                                     DHSRLQVKDSTIYVGDSWKPEE--NFVSATDKTGQDVPFE----KITVSGQVDNXKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGSERTLQSSKNQFLVNARNDSFDSLSVRTKIPAGA--DVLFDIYDVSN--DQVDSIYPQ
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ilarity 21.1%;
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Pred. No. 0.017
04; Mismatches
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nes 326;
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RESULT 11
ABU13708
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                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis, EF040, and the polypeptides encoded by them. The polypeptides are useful in detecting E. faecalis, as epitope tags, as molecular weight markers on SDS-PAGE gels or for molecular sleve gel filtration columns, in generating antibodies that specifically bind to the E. faecalis polypeptides, in generating an immune response against to faecalis and other Enterococcus species and as vaccines against other bacterial genera. The polynucleotides are useful as probes for gene mapping and for identifying E. faecalis in biological samples. Sequences ABU13508-ABU1375 represent EF040 polypeptides of the invention.

Note: The sequence data for this patent can also be obtained from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New EF040 puseful for
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14-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1998;
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VIKFTTPITNEIQIPIGFNYVPDSLPKDKSIPVDTIPITMSAEGLTPVDTTVTT---NSK
                                                    ELNQKLRAVMYNGHPQNANGIMEGLE-----PLNAIRVTQEAVWYYSDNAPISNPDESFK
                                                                                                                                                         --VNLEGSRSYQVYCFNLKKAFP----LGSDSSVKKWYKKHDGISTKFEDYAMSPRITGD
                                                                                                                                                                                                              SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ------NGAYSSR
                                                                                                                                                                                                                                                                   ALVTSMVGAKTVFGLVES---STPNAINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLR
                                                                                                       TTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYYK---
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r generating an immune response against E. faecalis and oth
cus species, and as vaccines against other bacterial genera
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97US-066009P.
97US-066099P.
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Pred. No. 0.017;
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Chakraborty T, Domanu ,
Chakraborty T, Baquero
Perez-Diaz J, Baquero
                                                                                                                                                                                                                                                                                                                              Antibacterial; vitamin B12; b
                                                                            Dussurget O,
Daniels J,
                                                                                                          Buchrieser C,
                                                                                                                                                                       11-APR-2000;
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                                                            Dominguez-Bernal G,
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                                                                                                                                                                                                                                                                                                Listeria monocytogenes
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PASTEUR.

2, Frangeul L, Couve E, Rusniok C, Fsini ..,
Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart ..
Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
Goebel W, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
Amend E, Charbit A, Durant L;
Figure P, Charbit A, Durant L;
Figure P, Comez-Lopez N;
Figure P, Hain T, Portillo F, Gomez-Lopez N;
Figure P, Haif J;
                                                                                                                                                                       2000FR-0004629
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bacterial infection; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate i. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by I monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fit, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific, antibodies, identification of L. monocytogenes and related organisms, an for biosynthesis and biodegradation, especially biosynthesis of Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                               VTIENTEQTGSVVLLKEDSATKD---AIAGAEFELQNADGTKVADNLVSNAD--GKIEVT 1152
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                                                                                                                       -EAAVIVTKENTAKTGSVVLTKEDSVSKATLSGAEFELQNAT----
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                       monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific
                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
                                                                                                                                              monocytogenes
it are useful
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                                                                                                                                                                                                                                                                                                                                          omic sequence for Lister prevention of Listeria
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                                                                                                           Invention relates to the genome sequence of Listeria to the SED-e (see ABA03041). The genome sequence and fragments ul for selecting probes and primers for detecting genes in es and related organisms, and for studying genetic
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Pred. No. 0.045;
8; Mismatches 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, for the present invention or antibodies of the present invention or antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6;
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                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
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                                                                                                                                          LKSISANNKITGNFSLVKTLPELHTLEV
  DKGDKYNKGYONLLSGGLVPTKPPTPGDPPMPPNOPQTTSVLIRKYAIG---DYSKLL---
                                                                                                                                                                                     LRAVMYNGHPQNAN-GIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRESESNLV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                   rnotorhabdus luminescens; TcdA; Southern corn rootworm; meal boll weevil; turf grub; Coleonfara: hardwarm; meal boll weevil; turf grub; turf grub; coleonfara: 
                                                                                                                                                                                                                                                                                                                                                                                                                  cabbage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW17900 standard; Protein; 1849
                                                                Peptide
                                                                                                                                                                                                                                                                                                                            Photorhabdus
                                                                                                                  Peptide
                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                       Diptera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photorhabdus luminescens insect toxin TcdAii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1998
                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283
                                                                                                                                                                                                                                                                                                                                                                                             looper; codling moth; corn earworm; European corn borer;
hornworm; tobacco budworm; Lepidoptera; Hymenoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YREKGQAIEY --- SGLTETQLRA----- ATQL--- AIYYFTDSAELDKDKLKDYHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIHLENLPAVKNLDISSNELTRLPKINDFPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTVKTDKTNLEFKDGKATI-----NLKHGESLTLQG-LPEGYSYLVKETDSEGYKVKVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYDQDLNIHMDLSKVDTSK---PGSYEVTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSKSGASSDPIKLSVKIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVNSNDISFEVGTELTSEVLLAKSGAVVTDLYDEAIKMEVDLSEVDSSKLGTYEATIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLKSPPDSEDGGKTMTPDFTTGEVKYTHIAGRDLFKYTVKPRDTDPDTFLKHIKKVIEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFLQDIRASASENAQITSDYS-----EVVDFATPGDYTVTLHAKNE-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANSSGVFEETRQTIQYIYVKDIINPEFPVYSENNVTPELPSNNNNSVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITVKVPEARI - - - - GKITIQYMDSENNELAESNTITGEVGETYETLAKEI - - EGYTLKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHPEDL---VDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEIELKNNKQELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FGDMNDSTLAVAKILVEYAQDSNPP--QLTDLDFFIPNNNKYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGLSKVSYTFDEVINSPAIAGKYTGTVNQPIEVKA----VPVIVADKSVSYAPVNAKDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IELSDGTYTLTE-LNSPA-----GYSIAEPITFKVEAGKVYTIIDGKQIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLATLNADKQAVTLSKTIAAGNFTIPNNVENLAGQMVTPKIISNNGTYSDQSIAWASGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                        turf grub; Coleoptera; beet armyworm; black cutworm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                            luminescens strain
                                                                     /note= "t
993..1004
                                                                                                                    466..475
                                                                                                                                                                 196..21
                                               /note= "isolated N-terminal peptide (Claim
                                                                                                                                          /note=
                                                                                                                                                                                     /note= "S2 N-terminus (Claim 30)"
                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EVANATVS----KTGITSDETLAFENNKEPVVPTGVDQKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - NPNKETVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVVYCFNA
                                                                                                                                                                                                                                                                                                                                                                          Acarina;
                                                                                     "tryptic
"tryptic
                                                                                                                                       "tryptic
                                                                                                                                                                                                                                    TcdAii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pest control; biological
                                                                                                                                                                                                                                                                                                                            W-14
  peptide (Claim
                                                                                        peptide (Claim 30)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DTEKPIIQINNPEIIIEKGSELTEGQIIDQVGITATD
                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southern corn rootworm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GDNVNSFQA---
                                                                                                                                       (Claim
                                                                                                                                                                                                                                                                                                                               55397).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LTTINVRSNKIDRLESSKLVDVP
                                                                                                                                          30)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RVFSSNDI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YTEDSSGNRSETVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPVTVVVHINDIQKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises the 209.2 kDa TcdAii insecticidal toxin protein of Photorhabdus luminescens W-14. Its sequence was deduced from a genomic DNA clone (AAT68844) and includes N-terminal and tryptic peptide sequences obtained from the isolated protein.

TcdAii is a proteolytic cleavage product of TcdA (see AAW17899).

Claimed toxins of P. luminescens (see AAW17871, AAW17894-89).

CAAW17899-900, AAW18301-06) can be produced by recombinant DNA methods and applied to, or genetically engineered into, insect larvae food and plants for insect control. The toxins are particularly effective against Southern corn rootworm, Colorado potato beetle, Western corn rootworm, meal worm, boll weevil and turf grub (Coleoptera), beet armyworm, black cutworm, cabbage looper, codling moth, corn earworm, (Lepidoptera), and are also active against insects of the orders (Lepidoptera, Diptera, Dictyoptera, Acarina and Homoptera. (All
                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%; Score 154; DB 18; Length 1849; Best Local Similarity 18.3%; Pred. No. 0.085; Matches 148; Conservative 120; Mismatches 287; Indels 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-1996;
06-NOV-1995;
28-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Photorhabdus sp. insecticidal protein toxins and DNA encoding them can be genetically engineered into insect larvae food and plants for insect control \ ^{\bullet}
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 34; Page 201-208; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blackburn MB, Bowen DJ, Ciche TA, Ensign JC, Ffrench-Constant RH, Guo L, Hey TD, Merlo DJ, Petell J, Roberts JL, Rocheleau TA, Schoonover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT68844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-281022/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strickland JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WISC ) WISCONSIN ALUMNI RES FOUND.
1034 YWRSVDHSKFNDGKFAANAWSEWHKIDCPINPYKSTIRPVIYK---SRLYLLWLEQKEIT 1090
                                     335
                                                                        974
                                                                                                                                                                                                                                                                                                                           157
                                                                                                          296
                                                                                                                                             914
                                                                                                                                                                               247
                                                                                                                                                                                                                  855
                                                                                                                                                                                                                                                      209
                                                                                                                                                                                                                                                                                   796 AQQLAVAPQGVSALV-GLDYIQSMKETPTYAQWENAAGVLTAGLNSQQANTLHAFLDESR 854
                                                                                                                                                                                                                                                  SNLVST---SQLSLMRQALKQ------LIDPNLA----TKMPKQVPDDFQL-----
                                                                                                                                                                                                                                                                                                                         AVMYNGHPQNANGIMEGLEPLNAIRVTQE-AVWYYSD-----NAPISNPDESFKRESE
                                                                    QSVSQSQLNADTVEDAFMSYLTSFEQVANLKVISAYHDNINNDQGLTYFIGLSETDAGEY 1033
                                                                                                                                                                                                                SAALSTYYIRQVAKAAAAIKSRDDLYQYLLIDNQVSAAIKTTRIAEAIA-SIQLYVNRAL
                                 -----RIELSDGTYTLT-----ELNSPAG--YSIAEPITFKVEAGKVYTI-IDGKQIE 379
                                                                                                        RKYA-----SUDIGE- 334
                                                                                                                                         ENVEENANSGVISRQFFIDWDKYNKRYSTWAGVSQLVYYPENYIDPTMRIGQTKMMDALL 973
                                                                                                                                                                             -SIFESEDKG------DKYNKGYQNLLSGGLVPTKPPTPGDPPMPPNQPQTTSVLI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                       1849 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0705484.
95US-0007255.
96US-0608423.
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/note= "tryptic peptide (Claim 30)"
1532..1554
/note= "claimed peptide (Claim 30)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fatig R;
, Orr GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                            Indels 254;
                                                                                                                                                                                                                                                                                                                                                            Gaps
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ОУ	ОУ	Qу	Qу	Q y	Qy	Qу	Qу	Qy Db
y 719 PVVPTGVDQKINGYLALIVIAGISLGIWG 747	y 663 ESLTLQGLPEGYSYLVKETDSEGYKVKVNSQEVANATVSKTGITSDETLAFENNKE 718	y 627TIELKNNKQELLSQTVKTDKTNLEF-KDGKATINLKHG 662 : : : : : : 1434 SPSFDEMNYQFNALEIDGSGLNFINNSASIDVTFTAFAEDGRKLGYESFSIPVTLKVSTD 1493	y 583 -HPEDLVDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFE 626 	y 532 YHGFGDMNDSTLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQW 582	y 476 DTFLKHIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKD 531 ::	y 447 475 b 1202 SYQQFDTNNVRRVNNRYGWGDYYLSMVYNGDDYVWGDYYLSMVYNGDIPTINYKAASSDL 1261	y 412 YYAKNKNGSSQVVYCFNADLKSPDDSEDGGKTMTP 446	y 380 NPNKETVEPYSVEAYNDFEEFSVLTTQNYAKF 411
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